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us-10-006-867-2.rup

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GenCore version 5.1.6
. Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

January 4, 2005, 12:03:24; Search time 189 Seconds (without alignments) 809.787 Million cell updates/sec

US-10-006-867-2 1392 1 MWWFQQGLSFLPSALVIWTS......YDTAPCPINNERTRLLSRDI 266 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

Total number of hits satisfying chosen parameters:

2000000000 Minimum DB seq length: Maximum DB seq length:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

'UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SOMMERES	
Result No.	Score	Query Match	Length	DB	ID	Description
п	1392	100.0	 	7	Qeuxes	Q6ux65 homo sapien
8	1392	100.0	266	7	AAQ88856	
ო	1245	89.4	267	~	Q9CR48	Q9cr48 m mus muscu
4	1235	88.7	267	~	Q9D520	Q9d520 mus musculu
Ś	1078	77.4	208	7	Q86VD3	Q86vd3 homo sapien
9	805.5	57.9	180	~	Q9D835	mus n
7	764.5	54.9	272	~	0EIQI0	Q6iqi0 brachydanio
80	764.5	54.9	272	~	AAH71426	Aah71426 brachydan
σ	725	52.1	136	~	Q8NBQ4	рошо
10	492.5	35.4	238	~	Q8N682	
11	479.5	34.4	238	~	Q9DC58	Q9dc58 mus musculu
12	•	34.4	238	~	BAB23366	Bab23366 mus muscu
13	•	33.9	287	~	Q6NRS6	Q6nrs6 xenopus lae
14	•	•	287	~	AAH70646	Aah70646 xenopus l
15	439.5	31.6	238	~	Q8QGB2	Q8qgb2 oncorhynchu
16	388.5		282	~	Q7QE61	
17	361.5	•	246	~	077262	
18	318.5	22.9	252	~	Q86 <i>F</i> 93	
19	288		271	~	093319	Q93319 caenorhabdi
20	262	18.8	238	~	Q8R218	
21	251.5	18.1	181	~	Q6XHF5	Q6xhf5 drosophila
22	251.5	•		~	AAR10251	Aar10251 drosophil
23	251	•		~	O9NUN1	Q9nunl homo sapien
24	251	•	132	~	AAH13773	Aah13773 homo sapi
25	240	•	132	~	Q78J26	Q78j26 mus musculu
26	203	14.6	249	7	Q8C8S3	Q8c8s3 mus musculu
27	201.5	•	271	7	Q6GPL4	Q6gpl4 xenopus lae
28	191.5	•	257	~	Q61QJ3	Q6iqj3 brachydanio
29	191.5	13.8	257	~	AAH71413	
30	185.5	13.3	219	7	Q6P6P1	Q6p6p1 mus musculu
31	185.5	13.3	219	7	AAH62109	Aah62109 mus muscu

Q7sxk4 brachydanio Q86ik0 dictyosteli	Q8c919 mus musculu Q86tg1 homo sapien	Qaqzea rattus norv Aah72517 rattus no		Q86kl7 dictyosteli O23135 caenorhabdi	Q9u3j7 caenorhabdi	Cab62801 caenorhab	Q8k117 mus musculu	Q6cd85 yarrowia li	029749 archaeoglob
Q7SXK4 Q861K0	Q8C9L9 Q86TG1	Q9Q289 AAH72517	091WN2	Q86K17 O23135	090337	CAB62801	Q8K117	Q6CDS5	HMEC_ARCFU
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294 243	123 271	271	271	2 4 2 4 3 8 4 4	252	252	140	299	332
13.2	11.6	11.3	10.9	10.8 8.6	8.1	8.1	7.7	7.4	7.4
183.5	161.5	157.5	151.5	150.5	112.5	112.5	106.5	103	103
32 33	ው ው (4 ሺ (3.5 3.7	38	w 4 w 0	41	42	43	44	45

ALIGNMENTS

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one:D730039I03 product:hypothetical protein, full insert
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                                                                                                                                                                                                                                                                                       "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: Bioinformatics Assessment."; Genome Res. 13:2265-2270(2003).
                                                                                                                                                                       SEQUENCE FROM N.A.
PubMed=12975309;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd J. Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D. Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.;
                                               AAQ88856 PRELIMINARY; PRT; 266 AA.
AAQ88856;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
WWFQ154.
UNQ154.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
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A; 29766 MW; 4F91D5C212D458E5 CRC64;
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Pred. No. 5.7e-108;
0; Mismatches 0;
 266
DTAPCPINNERTRLLSRDI
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Genome Res. 13:226
EMBL; AY358492; AA
SEQUENCE 266 AA;
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Best Local Similarit
Matches 266; Conse
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STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongue, and Whole body;

X MEDLINE=20530913; PubMed=11076861;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Rujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
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STEAIN=C57BL/6J; TISSUE=Tongue, and Whole body;
Adachi J., Alzawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshino M.,
                                                                                                                      Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/6J; TISSUB=Mammary gland;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
                                                                                                                                                                                                                                                                                                                     Tongue, and Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Whole body;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tongue,
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Mammary gland, Tongu.
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Mammary gland, MEDLINE=21085660; PubMed=11217851; FIKEN FANTOM Consortium; "Functional annotation"
Bequence).
Name=2610318G18Rik;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Hayashizaki
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COSOS20;
COSOS20;
T 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
T 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
T 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
T 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
E Mus musculus adult male testis cDNA, RIKEN full-length enriched
E library, clone:4930524M19 product:hypothetical protein, full insert
E sequence.
N Name=2610318G18R1k;
S Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,

Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AK012044; BAB27990.1; -.

R EMBL; AK052824; BAC35162.1; -.

R MGD; MGI:1914421; 2610318G18Rik.

W Hypothetical protein.

O SEQUENCE 267 AA; 30227 WW; 228214D5AFF36783 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                ATIYVRYKQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAA
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                                                                                                                                                                                                                                                                  Query Match 89.4%; Score 1245; DB 2; Length 2 Best Local Similarity 86.4%; Pred. No. 1e-95; Matches 229; Conservative 19; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
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TVPCPVNNERTPLLSRD
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSOLTIUM;
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Nature 409:685-6
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Arakawa T., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Arakawa T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Kato H.,

Kawai J., Kojima Y., Itoh M., Izawa M., Koya S., Kurihara C.,

A Awai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A Awai J., Kojima Y., Itoh M., Nishi K., Nomura K., Numazaki R., Ohno M.,

A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

A Sano H., Sasaki D., Shibata K., Shibata Y., Takahashi F., Tanaka T.,

A Sogabe Y., Zuzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

A Pejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

A Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AKO15888; BAB30020.1; -.

MGD; MGI:1914421; 2610318G18Rik.

W Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUB-Testis;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                             of
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=20530913; PubMed=11076861;
A Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKEN integrated sequence analysis (RISA) system-384-format genome Res. 10:1757-1771(2000).
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                                Phase I & II
on functional
                        the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
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Q9D835
ID Q9D835
AC Q9D835;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2004 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Mus musculus adult male small intestine cDNA, RIKEN full-length
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TISSUE=Eye;
Strausberg R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC047025; AAH47025.2; -.
SEQUENCE 208 AA; 23352 MW; 35788E00AE9E4B35 CRC64;
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100.0%; Pred. No. 6.7e-82;
iive 0; Mismatches 0;
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Matches 208; Conservative
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the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
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STRAIN=C57BL/6J; TISSUE=Small intestine;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai Y.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                     protein, full
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STRAIN=FVB/N; TISSUE=Kidney;
STRAIN=22388257; PubMed=12477932;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUB=Small intestine;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
      SN14 product: hypothetical protein).
                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUB=Small intestine;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Small intestine;
The FANTOM Consortium,
      clone:2010305N14
library, clone:
                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                        insert sequence (261)
Name=2010305N14Rik;
Mus musculus (Mouse)
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Query Match
Best Local Similarity 55.2%
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak B.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
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OGIQIO;
OGIQIO;
OS-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
29c:86754.
Name=zgc:86754;
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostel; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87;
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Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
Strausberg R.;
Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK008532; BAB25725.1; -.
EMBL; BC024458; AAH24458.1; -.
MGD; MGI:1919359; 2010305N14Rik.
Hypothetical protein.
SEQUENCE 180 AA; 20324 MW; 7952C2302D9235DF CRC64;
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|TVPCPVNNERTPLLSRD 178
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Best Local Similarity
Matches 159; Conserv
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TISSUE=Embryo;
MEDLINE=22388257;
Strausberg R.L., F
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A ltschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.;
I "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIAAVLCIATIYVRYKQVHALSP-EENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 AHVSGAVLTFGMGSLYMFVQTILSYQMQPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSV
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01-JUN-2004 (TrEMBLrel. 27, Created)
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii, Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC071426; AAH71426.1; -.
SEQUENCE 272 AA; 30362 MW; B7FE8BDD89FC87FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
Generation and initial analysis of more than 15,000 full-length human
R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIAAVLCIATIYVRYKQVHALSP-EENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFA 119
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Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y., Nagahari K., Sugano S., Isogai T.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK075350; BAC11562.1; -. SEQUENCE 136 AA; 15728 MW; 984FEDC29636ACOC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.9%; Score 764.5; DB 2; Length 55.2%; Pred. No. 1.2e-55; ive 48; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
TISSUE=Embryo;
Strausberg R.;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC071426; AAH71426.1; -.
Hypothetical protein.
SEQUENCE 272 AA; 30362 MW; B7FE8BDD89FC87FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8NBQ4 PRELIMINARY; PRT; 136 AA.
Q8NBQ4;
Q8NBQ4;
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein PSEC0031.
Hypothetical protein PSEC0031.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bute Mammalia; Butheria; Primates; Catarrhini; Hominidae; Hom NCBI_TaxID=9606;
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Best Local Similari
Matches 138; Cons
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MYSTLPGV
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08NBQ4
1D Q81
AC Q81
DT 011
DT 011
DD OC EUI
OC EUI
OC MAI
RR C11
RRA SEI
RRA
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Length 136;

52.1%; Score 725; DB 2; 1 100.0%; Pred. No. 1.2e-52;

Query Match Best Local Similarity

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TISSUE-Liver;

XC TISSUE-Liver;

XX MEDLINE=22388257; PubMed=12477932;

XA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

XA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,

RA Altschul M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Raha S.S., Loquellano N.A., Sodergran E.J., Lu X., Gibbs R.A.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevhenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human mand and initial analysis of more than 15,000 full-length human mand mand in the second second
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                                           131 MGSLYMFVQTILSYQMQPKIHGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLE
                                                                            QKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLTLYDTA
                                                                                                                                                                     61 QKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLTLYDTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MWWFOOGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 35.4%; Score 492.5; DB 2; Length Local Similarity 38.8%; Pred. No. 5.1e-33; Les 97; Conservative 53; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue=Live,
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC018435; AAH18435.1; -.
InterPro; IPR000504; RNA_rec_mot.
PROSITE; PS00030; RRM RNP_1; UNKNOWN 1.
SEQUENCE 238 AA; 26253 WW; 511875677737F6C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
     ö
     Mismatches
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   ö
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01-OCT-2002 (TrEMBLrel. 2:
01-MAR-2004 (TrEMBLrel. 2:
FLJ11259 protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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 KTTLFAAHVSGAVLTFGMGSLYMFVQTILSYQMQPKIHGKQVFWIRLLLVIWCGVSALSM 173
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

X STAIN=C57BL/6J; TISSUE=Lung;

X MEDLINE=20530913; PubMed=11076861;

X Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Andrawa J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Avamanoto H., Ishii Y., Nakamura S., Hazawa M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., A Yamamoto R., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Tanaka T., Genome Res. 10:1757-1771(2000).
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STRAIN=C57BL/6J; TISSUE=Lung;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
               ELAVPUVHDGGALLAFUCGVUYTLLQSIISYKSCPQWNSLSTCHIRMVISAVSCAAVIPM
                                                   LICSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAABWSMSFSFFGFFLTYIRDFQKI
                                                                  --TKLEWNPREKDYVYHVVSAICEWTVAFGFIFYFLTFIQDFQSV
                                                                                                                                                                                            Q9DC58
Q9DC58;
Q9DC58;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 20, Last annotation update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched library, clone:1200002N14 product:hypothetical RNA-binding region RNP-1 (RNA recognition motif) containing protein, full insert sequence.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ation of a full-length mouse cDNA collection."; 0(2001).
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STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-16
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TLRISTEI
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STRAIN-CSTBL/GJ; TISSUB-Lung;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Anagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
A magaki T., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Kogabe Y., Suzuki H., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
A Muramatsu M., Hayashizaki Y.,
B Muramited (Jul-2000) to the EMBL/GenBank/DDBJ databases.
B Muramatsu M., Hayashizaki Y.,
B Muramatsu M., Hayashizaki M.,
B Muramatsu M., Hayashizaki M.
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
Adult male lung cDNA, RIKEN full-length enriched library,
clone:1200002N14 product:hypothetical RNA-binding region RNP-1 (RN
recognition motif) containing protein, full insert sequence.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Musin
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37.3%; Pred. No. 6.2e-32;
tive 56; Mismatches 79;
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
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STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=21085660; PubMed=11217851;
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TLRISTEIN 235
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SEQUENCE FROM N.A.
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RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M., Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Koyima Y., Konno H., Kouda M., Koya S., Kurihara C., RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., RA Okazaki Y., Okido T., Owa C., Saito R., Sato R., Sasaki D., Shibata K., Shibata Y., Salu K., Yoshida K., Yoshido M., RA Muramatsu M., Hayashizaki Y., Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO04552; BAB23366.2; --
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                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

SABIDATA K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sawaluchi S., Ikegami T., Tashiro H., Itoh M., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Rakiki Y.; RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
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               full-length mouse cDNA collection.";
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                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=99279253; PubMed=10349636;
A Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
"...k Enzymol. 303:19-44(1999).
                 æ
  M Consortium;
annotation of a
685-690(2001).
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             "Functional ann
Nature 409:685-
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TISSUE-Liver;

WEDLINE=22388257; PubMed=12477932;

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahy J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Riczywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human and man a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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TISSUE=Liver;
MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
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                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
LOC431986 protein (Fragment).
Name=LOC431986;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                            PRT;
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Klein S., Strausberg R.;
Submitted (MAY-2004) to the
EMBL; BC070646; AAH70646.1;
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Best Local Similarity 38.0
Matches 93, Conservative
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227 TLRISTEIN 235
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Best Local S
Matches 96
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TISSUE=Liver;

X MEDLINE=22341132; PubMed=12454917;

X MICHARDAN S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

Richardson P.,

Tinitiative.", and genomic tools for Xenopus research: The NIH Xenopus

Richardson P.,

Tinitiative.", Dev. Dyn. 225:384-391(2002).

XI Initiative.", Dev. Dyn. 225:384-391(2002).

XI Initiative.", Dev. Dyn. 225:384-391(2002).

XI INITIALINE=2388257; PubMed=12477932;

XI SEQUENCE FROM N.A.

XI SEQUENCE T. MARCHAR N.A.

XI SEQUENCE FROM N.A.

| | : | | : | | : | : | : | : | : | | : | | | PAVHDAGALITPICGVMYILLQSYISYKSCPTWNTRATCHIRMTVSLIAFIAVVPMSVFS
                                                                                  SVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYIRDFQKISLRV
                                                                                                                    AAH70646 PRELIMINARY; PRT; 287 AA.
AAH70646;
13-MAY-2004 (TrEMBLrel. 27, Created)
13-MAY-2004 (TrEMBLrel. 27, Last sequence update)
13-MAY-2004 (TrEMBLrel. 27, Last annotation update)
13-MAY-2004 (TrEMBLrel. 27, Last annotation update)
13-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein (Fragment).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
NCBI_TaxID=8355;
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y 38.0%; Pred. No. 3.5e-31;
rrvative 56; Mismatches 79;
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Submitted (MAY-2004) to the EN
EMBL; BC070646; AAH70646.1; -
Hypothetical protein.
NON TER 1
SEQUENCE 287 AA; 31871 MW;
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Best Local Similarity
Matches 93; Conserv
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STEIH 28
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TISSUE=Liver;
                                                                                                                                                                                            EANLH 24
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3 WFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI

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177
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                                                                                                  178 SVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLTYIRDFQKISLRV
                                                                                                                                                                                                                                                                                   1 MWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         080GB2;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
VHSV-induced protein-6.
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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O'Farrell C., Vaghefi N., Cantonnet M., Buteau B., Boudinot Benmansour A.;

"Survey of transcript expression in rainbow trout leukocytes major contribution of interferon-responsive genes in the ear response to a rhabdovirus infection.";

J. Virol. 76:8040-8049(2002).

EMBL; AF483532; AAM18471.1; -.

SEQUENCE 238 AA; 26650 MW; 06BEDE247670D134 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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le : 192 secs
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